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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT: MATZUK ET AL. : DOCKET NO. P01925US1
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TITLE: OVARY-SPECIFIC GENES :
AND PROTEINS : :

Assistant Commissioner of Patents
Washington, D.C. 20231

FIRST PRELIMINARY AMENDMENT

Dear Sir:

Please enter the following amendments to the claims prior to the examination of the application.

In the drawings:

Please replace Figures 1 through 14 of the PCT published application (12 sheets) with the substitute Figures 1 through 14 transmitted herewith (15 sheets). Figures 1 through 6 have been separated onto individual pages and Figure 13 has been separated into Figure 13A and Figure 13B.

In the specification:

Please replace the paragraph beginning at page 4, line 2, with the following rewritten paragraph:

--FIG. 1 shows the 1276 base pair cDNA sequence of gene O1-180 (SEQ ID NO: 1).--

Please replace the paragraph beginning at page 4, line 3, with the following rewritten paragraph:

--FIG. 2 shows the 361 amino acid sequence that is coded for by gene O1-180 (SEQ ID NO: 2).--

Please replace the paragraph beginning at page 4, line 4, with the following rewritten paragraph:

--FIG. 3 shows the 1817 base pair cDNA sequence of gene O1-184 (SEQ ID NO: 3).--

Please replace the paragraph beginning at page 4, line 5, with the following rewritten paragraph:

--FIG. 4 shows the 426 amino acid sequence that is coded for by gene O1-184 (SEQ ID NO: 4).--

Please replace the paragraph beginning at page 4, line 6, with the following rewritten paragraph:

--FIG. 5 shows the 1019 base pair cDNA sequence of gene O1-236 (SEQ ID NO: 5).--

Please replace the paragraph beginning at page 4, line 7, with the following rewritten paragraph:

--FIG. 6 shows the 207 amino acid sequence that is coded for by gene O1-236 (SEQ ID NO: 6)--

Please replace the paragraph beginning at page 4, line 30, with the following rewritten paragraph:

--FIG. 10. Npm2 cDNA representation. Schematic representation of the mouse Npm2 cDNA sequence (984 bp) and two of the clones isolated from the mouse ovary CDNA libraries. The original 01-236 probe (749 bp) is shown at the top and encompasses the entire Npm2 open reading frame. The open reading frame (solid box) is 621 bp and the 5' UTR and 3' UTR sequences (thin lines) are 155 bp and 205 bp, respectively. The polyA sequences are not depicted. Clone 236-1 was isolated from the wild-type ovary cDNA library and clone 236-3 was isolated from the GDF-9-deficient ovary cDNA library. Clone 236-3 (984 bp excluding polyA sequence) is 4 bp longer at the 5' end and 1 bp longer at the 3' end than clone 236-1 (979 bp

excluding polyA sequences). Codon 36 of the open reading frame of both cDNAs is GGC (Glycine; Figure 11) whereas the same codon of the 129SvEv gene is TGC (Cysteine; Figures 13A and 13B (SEQ ID NO: 7 through SEQ ID NO: 14)).--

Please replace the paragraph beginning at page 5, line 28, with the following rewritten paragraph:

--FIGS. 13A and 13B. Mouse Npm2 gene (SEQ ID NO: 7 through SEQ ID NO: 14) and amino acid sequences. Uppercase letters represent sequence identity with the Npm2 cDNA sequences; non-transcribed 5' and 3' sequences and intron sequences are shown in lowercase. The predicted transcription initiation codon, the termination codon, and the polyadenylation signal sequence are all underlined. Numbers along the left side represent the amino acids. The underlined and bolded “T” in codon 36, the bolded “c” for amino acid 26, and the underlined and bolded “C: in the 3' UTR sequence indicate differences between the cDNA and gene sequences. Arrows indicate where the O1-236 fragment initiates and ends in the cDNA sequence.--

Please replace the paragraph beginning at page 10, line 15, with the following rewritten paragraph:

--Fragments of proteins are seen to include any peptide that contains 6 contiguous amino acids or more that are identical to 6 contiguous amino acids of either of the sequences shown in Figures 2 (SEQ ID NO: 2), 4 (SEQ ID NO: 4), 6 (SEQ ID NO: 6), 11 and 14. Fragments that contain 7, 8, 9, 10, 11, 12, 13, 14 and 15 or more contiguous amino acids or more that are identical to a corresponding number of amino acids of any of the sequences shown in Figures 2 (SEQ ID NO: 2), 4 (SEQ ID NO: 4), 6 (SEQ ID NO: 6), 11 and 14 are also contemplated. Fragments may be used to generate antibodies. Particularly useful fragments will be those that make up domains of O1-180, O1-184 or O1-236. Domains are defined as portions of the proteins having a discrete tertiary structure and that is maintained in the absence of the remainder of the protein. Such structures can be found by techniques known to those skilled in the art. The protein is partially digested with a protease such as subtilisin, trypsin, chymotrypsin or the like and then subjected to polyacrylamide gel electrophoresis to separate the protein fragments. The fragments can then